CLAIMS:

1. A method of performing real-time infection control over a computer network, comprising:

   obtaining a sample of a microorganism at a remote facility;

   sequencing a first region of a nucleic acid from the microorganism sample;

   comparing the first sequenced region with historical sequence data stored in a database;

   determining a measure of phylogenetic relatedness between the microorganism sample and a plurality of historical samples stored in the database; and

   providing infection control information based on the phylogenetic relatedness determination to the remote facility, thereby allowing the remote facility to use the infection control information to control or prevent the spread of an infection.

2. The method of claim 1, wherein the infection control information is transmitted to the remote facility over a computer network.

3. The method of claim 2, wherein the database is a centralized database located in an infection control facility, the infection control facility transmitting infection control information to the remote facility via a computer network.

4. The method of claim 1, wherein the database is located in the same location as the remote facility.

1   5. The method of claim 1, wherein the first region that is sequenced is a region that has

2   been identified to have a mutation rate which is suitably fast for performing real-time

3   infection control.

1   6. The method of claim 4, wherein the first region that is sequenced is a repeat region.

1   7. The method of claim 6, wherein the microorganism is *Staphylococcus aureus* and the

2   first region is located in the protein A gene or the coagulase gene.

1   8. The method of claim 7, wherein a sample of a microorganism is obtained from a

2   patient before the patient is admitted to the health care facility.

1   9. The method of claim 1, wherein the microorganism is a bacterium, virus, or fungus.

1   10. The method of claim 1, further including:

2   obtaining a medical history from a patient from which the microorganism sample

3   was taken;

4   determining an infection risk factor based on the patient's medical history, the

5   infection risk factor being a measure of the patient's risk of acquiring an infection; and

6   taking appropriate infection control measures in accordance with the infection risk

7   factor.

1 11. The method of claim 10, further including:

2   transmitting the patient's medical history to the centralized database without

3 transmitting sensitive patient information; and

4   storing the sensitive patient information in a local database at the health care

5 facility.

1 12. The method of claim 1, wherein the step of sequencing comprises either:

2   a) sequencing the microorganism sample at the remote facility and transmitting

3 the resulting sequence data to the centralized database via a computer network; or

4   b) sending the microorganism sample to an infection control facility associated

5 with the centralized database, sequencing the microorganism at the infection control

6 facility, and storing the sequence data in the centralized database.

1 13. The method of claim 1, wherein the first region is identified by a set of primers.

1 14. The method of claim 1, wherein the first region is amplified prior to sequencing.

1 15. The method of claim 1, wherein the step of determining the phylogenetic relatedness

2 between the microorganism sample and a historical sample stored in the database

3 includes one of the following:

4   a) calculating a relative cost between the two samples; or

5   b) calculating an absolute cost for each sample and comparing the absolute costs.

1   16. The method of claim 1, wherein the step of determining the phylogenetic relatedness

2   between the microorganism sample and a historical sample stored in the database

3   includes:

4   identifying repeat sequences in the sequenced first region of the microorganism

5   sample and the historical samples; and

6   comparing the similarity between a repeat motif in the microorganism sample

7   sequence and a repeat motif in a corresponding historical sample sequence; and

8   determining a repeat motif cost that is a measure of phylogenetic distance

9   between the samples based on the similarity between the repeat motifs.

1   17. The method of claim 16, further including:

2   comparing the similarity between individual base-pair sequence in the

3   microorganism sample and the individual base-pair sequence in the corresponding

4   historical sample; and

5   determining a point mutation cost that is measure of phylogenetic distance

6   between the samples based on the similarity between the individual base pair sequences.

1   18. The method of claim 17, further including:

2   determining a total cost based on a weighted combination of the repeat motif cost

3   and the point mutation cost.

1   19. The method of claim 16, further including:

2   calculating a phylogenetic distance between the sample and a historical sample,

3   wherein the deletion or insertion of a repeat sequence is treated as a single event.

1   20. The method of claim 19, wherein a point mutation is treated as a single event.

1   21. The method of claim 1, wherein the step of determining the phylogenetic relatedness

2   between the microorganism sample and historical samples stored in the database includes

3   at least one of:

4   comparing to historical samples obtained from the same remote facility to

5   determining a local phylogenetic relatedness;

6   comparing to historical samples obtained from the same region to determine a

7   regional phylogenetic relatedness; and

8   comparing to global historical samples to determine a global phylogenetic

9   relatedness.

1   22. The method of claim 1, further including:

2   transmitting the physical location of a patient from which the microorganism

3   sample is taken;

4   storing the physical location in the centralized database; and

5   determining a path of transmission of an infection based on the phylogenetic

6   relatedness determination and the physical location of the patient.

1   23. The method of claim 22, further including:

2   storing a map of the health care facility in the centralized database; and

3   determining the spread of the infection based on the map of the health care

4   facility.

1   24. The method of claim 23, further including:

2   sensing the patient's physical location; and

3   transmitting the patient's physical location to the centralized server.

1   25. The method of claim 1, further including:

2   determining the virulence of the microorganism by retrieving the virulence data of

3   identical or similar microorganisms from the centralized database; and

4   transmitting virulence information to the remote facility.

1   26. The method of claim 1, further including:

2   determining drug resistance and treatment information by retrieving drug

3   information data of identical or similar microorganisms from the centralized database;

4   and

5   transmitting the drug information data to the health care facility.

1   27. The method of claim 1, further including:

2   determining whether the health care facility has a potential outbreak problem; and

3   transmitting an outbreak warning to the health care facility.

1   28. The method of claim 1, further including:

2   sequencing a second region of the nucleic acid of the microorganism sample; and

3   comparing the second sequenced region with corresponding historical sequence

4   data stored in a centralized database;

5   determining a measure of phylogenetic relatedness between the microorganism

6   sample and historical samples stored in the centralized database based on the comparison

7   of the second sequenced region.

1   29. The method of claim 28, wherein the determination of relatedness based on the

2   second sequenced region is used to verify the determination of relatedness based on the

3   first sequenced region.

1   30. The method of claim 28, further including:

2   identifying a first level of subspecies of the sample based on the first sequenced

3   region; and

4   identifying a second level of subspecies of the sample based on the second

5   sequenced region.

1   31. The method of claim 28, further including:

2   tracking the global spread of an infection based on sequencing and comparing a

3   slowly mutating region of the nucleic acid; and

4   tracking the local spread of an infection based on sequencing and comparing a

5   more rapidly mutating region of the nucleic acid.

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1 32. A system for performing real-time infection control over a computer network,

2 comprising:

3   a computer network;

4   a centralized database;

5   a remote facility connected to the computer network, the remote facility obtaining

6 a sample of a microorganism;

7   a server connected to the computer network, the server

8   receiving sequence data for a first sequenced region of a nucleic acid from

9   the microorganism sample,

10   accessing the centralized database and comparing the first sequenced

11 region with historical sequence data stored in the centralized database,

12   determining a measure of phylogenetic relatedness between the

13 microorganism sample and historical samples stored in the centralized database,

14 and

15   transmitting infection control information based on the phylogenetic

16 relatedness determination to the remote facility over the computer network,

17   thereby allowing the health care facility to use the infection control information to

18   control or prevent the spread of an infection.

1 33. Computer executable software code stored on a computer readable medium,

2 performing a method of real-time infection control over a computer network, comprising:

3   obtaining a sample of a microorganism at a remote facility;

4   sequencing a first region of a nucleic acid from the microorganism sample;

5   comparing the first sequenced region with historical sequence data stored in a

6   centralized database;

7   determining a measure of phylogenetic relatedness between the microorganism

8   sample and historical samples stored in the centralized database; and

9   providing infection control information based on the phylogenetic relatedness

10   determination to the remote facility, thereby allowing the remote facility to use the

11   infection control information to control or prevent the spread of an infection.